

OIEP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/881,636

DATE: 10/15/2001
TIME: 16:25:22

Input Set : A:\Seqlist.txt
Output Set: N:\CRF3\10152001\I881636.raw

ENTERED

```

4 <110> APPLICANT: Mary Faris
5      Rene S. Hubert
6      Daniel E.H. Afar
7      Elana Levin
8      Steve Chappell Mitchell
9      Arthur B. Raitano
10     Aya Jakobovits
12 <120> TITLE OF INVENTION: 55P4H4: GENE EXPRESSED IN VARIOUS
13     CANCERS
15 <130> FILE REFERENCE: 129.12USU1
17 <140> CURRENT APPLICATION NUMBER: 09/881,636
18 <141> CURRENT FILING DATE: 2001-06-13
20 <150> PRIOR APPLICATION NUMBER: 60/211,454
21 <151> PRIOR FILING DATE: 2000-06-13
23 <160> NUMBER OF SEQ ID NOS: 720
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 2610
29 <212> TYPE: DNA
30 <213> ORGANISM: Homo sapiens
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (204)...(784)
36 <400> SEQUENCE: 1
37 agccggcgca ggggtggccgg ggaggggtga gcaggggtgcc gctggctgct ggggtctgca 60
38 ggtcaccgag tccccaggag aggggactcc taagaagcca cctgcctgtg tttaccgggc 120
39 agcgagcgcg caggcccccg cgaactcctg gcagcgctca ggaaaggccg ttgcgcctcg 180
40 cgaaggaaac agagccgttg acc atg gtt gca act ggc agt ttg agc agc aag 233
41                               Met Val Ala Thr Gly Ser Leu Ser Ser Lys
42                               1           5           10
44 aac ccg gcc agc att tca gaa ttg ctg gac tgt ggc tat cac cca gag 281
45 Asn Pro Ala Ser Ile Ser Glu Leu Leu Asp Cys Gly Tyr His Pro Glu
46           15           20           25
48 agc ctg cta agt gat ttt gac tac tgg gat tat gtt gtt cct gaa ccc 329
49 Ser Leu Leu Ser Asp Phe Asp Tyr Trp Asp Tyr Val Val Pro Glu Pro
50           30           35           40
52 aac ctc aac gag gta ata ttt gag gaa tca act tgc cag aat ttg gtt 377
53 Asn Leu Asn Glu Val Ile Phe Glu Glu Ser Thr Cys Gln Asn Leu Val
54           45           50           55
56 aaa atg ctg gag aac tgt ctg tcc aaa tca aag caa act aaa ctt ggt 425
57 Lys Met Leu Glu Asn Cys Leu Ser Lys Ser Lys Gln Thr Lys Leu Gly
58           60           65           70
60 tgc tca aag gtc ctt gtc cct gag aaa ctg acg cag aga att gct caa 473
61 Cys Ser Lys Val Leu Val Pro Glu Lys Leu Thr Gln Arg Ile Ala Gln
62 75           80           85           90
64 gat gtc ctg cgg ctt tcc tca acg gag ccc tgc ggc ttg cga ggt tgt 521
65 Asp Val Leu Arg Leu Ser Ser Thr Glu Pro Cys Gly Leu Arg Gly Cys

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66          95          100          105
68 gtt atg cac gtg aac ttg gaa att gaa aat gta tgt aaa aag ctg gat 569
69 Val Met His Val Asn Leu Glu Ile Glu Asn Val Cys Lys Lys Leu Asp
70          110          115          120
72 agg att gtg tgt gat tct agc gtc gta cct act ttt gag ctt aca ctt 617
73 Arg Ile Val Cys Asp Ser Ser Val Pro Thr Phe Glu Leu Thr Leu
74          125          130          135
76 gtg ttt aag cag gag aac tgc tca tgg act agc ttc agg gac ttt ttc 665
77 Val Phe Lys Gln Glu Asn Cys Ser Trp Thr Ser Phe Arg Asp Phe Phe
78          140          145          150
80 ttt agt aga ggt cgc ttc tcc tct ggt ttc agg aga act ctg atc ctc 713
81 Phe Ser Arg Gly Arg Phe Ser Ser Gly Phe Arg Arg Thr Leu Ile Leu
82 155          160          165          170
84 agc tca gga ttt cga ctt gtt aag aaa aaa ctt tac tca ctg att gga 761
85 Ser Ser Gly Phe Arg Leu Val Lys Lys Lys Leu Tyr Ser Leu Ile Gly
86          175          180          185
88 aca aca gtg att gaa ggg tcc ta aaaagggaaa atatataaag attatttcat 814
89 Thr Thr Val Ile Glu Gly Ser
90          190
92 gattgggtag taaaactatt cagctagtca gctaaagtca tttgtagttt gccccacctg 874
93 ccctaaataa gaaaccccaa atgtagtctc ttttctttct gtgtttcaca ttcataagcaa 934
94 ctgcagctaa caggctgatt ttctggcctt tggagaagtg attcaaaata gtgtagattt 994
95 tctgcataga tcccattttt gtacagaatt gaatgggatg gaataggtaa gcaaagttag 1054
96 aagcccatit gagttttaca ttgtattcca caatttggtt tcaggtaggc ttggtgatag 1114
97 actatataaa ccagatttgc ctattttgat tttcatatgg cttttttttc tgtaagtttt 1174
98 cagaggattt tttaaatcac agaatcatac taaatgatat ttagcctatc aaaacttcca 1234
99 aaagcccaca ccaccagttc ctgactcaaa tttgaagggt ttttagacag gagggtagga 1294
100 ttaagtaggt gagtttaatt aaagcttaac ctaggtaag agtaaatgag aaatattacg 1354
101 gcaataatgg aactgcttca ctgtttcttg gtgacttctc cactctaag ttttaaagag 1414
102 gcaacaaaag cttatggtgc catttcagta accacggtgt tgtttttagat gcctttataa 1474
103 gctcagtttc ccttggtctt aagtgttgaa tactgtcttt aaactagaaa aatgcaaat 1534
104 attgaactga tatttctgtg tgtagtttat tactcttcca ttgagtgaat gatgaatacc 1594
105 tgtgaggata ggaaatgagt tctgagatct agtccctctc tgattcactt agtaatctat 1654
106 cctcttttca gtattacatg tgcttaatct cagatgaacc atttcaccat ggcagtgtta 1714
107 tctcatctct gggtttttct gggaattgaa gtatctctcc ttaaccccaa ttgtcaaggg 1774
108 tagtagctgt atactaccac tttgaattat tgaaacgggt caatttacga agtctgcatt 1834
109 ggctatggag atatggttta tagtacagcc tagagaatga aactcaccgt ccagataacc 1894
110 atgcatgcac ccagattttt tccaccttgg atacctgtca ctagggaata ataaaggcct 1954
111 gattttttgt cttattccaa ctaagtagat cattatctct ttcctttttt atgttaatga 2014
112 gagaatttag cctccactca acaatgttca attcagcaag gctttcatat ccttgctgtg 2074
113 ggtcgtggat aaggagctta ttcaggtttc ctgccctagc tattagctcc acttcacatg 2134
114 ctggagactg gcgtagggac agatgtattc atcctggtgt tactgaaaaa cagggtgtgat 2194
115 cctgttagtg atactataag tgacctaaaa tgtcactgtt caaattagca agtggttctaa 2254
116 caaactaaac tottcaaagt cttggaaaga tactacaaag ccaatcttta tagaattggg 2314
117 ccaagataaa tctatgttgt tttgcatggc tattgttaag ctccaaagg tcaactgtgtt 2374
118 tctgccgctg tcttgaggtt gtcaccactg actgggcaag gcttcttggg catggatgta 2434
119 gaactgttgt ccttttccca ctaacagtta tctttgactc tcttgctgtt tatgcttaca 2494
120 aaatggtgat ggcttatgga aggctgttaa attaatatc ctgttaaagg aaattaaagt 2554
121 ttgtctatit ttgacaataa aacattatat atttttaaaa aaaaaaaaaa aaaaaa 2610

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123 <210> SEQ ID NO: 2
124 <211> LENGTH: 193
125 <212> TYPE: PRT
126 <213> ORGANISM: Homo sapiens
128 <400> SEQUENCE: 2
129 Met Val Ala Thr Gly Ser Leu Ser Ser Lys Asn Pro Ala Ser Ile Ser
130 1 5 10 15
131 Glu Leu Leu Asp Cys Gly Tyr His Pro Glu Ser Leu Leu Ser Asp Phe
132 20 25 30
133 Asp Tyr Trp Asp Tyr Val Val Pro Glu Pro Asn Leu Asn Glu Val Ile
134 35 40 45
135 Phe Glu Glu Ser Thr Cys Gln Asn Leu Val Lys Met Leu Glu Asn Cys
136 50 55 60
137 Leu Ser Lys Ser Lys Gln Thr Lys Leu Gly Cys Ser Lys Val Leu Val
138 65 70 75 80
139 Pro Glu Lys Leu Thr Gln Arg Ile Ala Gln Asp Val Leu Arg Leu Ser
140 85 90 95
141 Ser Thr Glu Pro Cys Gly Leu Arg Gly Cys Val Met His Val Asn Leu
142 100 105 110
143 Glu Ile Glu Asn Val Cys Lys Lys Leu Asp Arg Ile Val Cys Asp Ser
144 115 120 125
145 Ser Val Val Pro Thr Phe Glu Leu Thr Leu Val Phe Lys Gln Glu Asn
146 130 135 140
147 Cys Ser Trp Thr Ser Phe Arg Asp Phe Phe Phe Ser Arg Gly Arg Phe
148 145 150 155 160
149 Ser Ser Gly Phe Arg Arg Thr Leu Ile Leu Ser Ser Gly Phe Arg Leu
150 165 170 175
151 Val Lys Lys Lys Leu Tyr Ser Leu Ile Gly Thr Thr Val Ile Glu Gly
152 180 185 190
153 Ser
157 <210> SEQ ID NO: 3
158 <211> LENGTH: 300
159 <212> TYPE: DNA
160 <213> ORGANISM: Homo sapiens
162 <400> SEQUENCE: 3
163 gatctatgca gaaaatctac actatthttga atcacttctc caaaggccag aaaatcagcc 60
164 tgtagctgc agttgctatg aatgtgaaac acagaaagaa aagagactac atttgggggtt 120
165 tcttatttag ggcaggtggg gcaaactaca aatgacttta gctgactagc tgaatagttt 180
166 tactacccaa tcatgaaata atctttatat attttccctt tttaggacctt ttcaatcact 240
167 gttgttccaa tcaagtgaagta aagttttttc ttaacaagtc gaaatcctga gctgaggatc 300
170 <210> SEQ ID NO: 4
171 <211> LENGTH: 7
172 <212> TYPE: DNA
173 <213> ORGANISM: Homo sapiens
175 <400> SEQUENCE: 4
176 accatgg
178 <210> SEQ ID NO: 5
179 <211> LENGTH: 176
180 <212> TYPE: PRT

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181 <213> ORGANISM: Ratus norvegicus

183 <400> SEQUENCE: 5

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184 Ser Leu Glu Ser Ser Asp Cys Glu Ser Leu Asp Ser Ser Asn Ser Gly
185 1 5 10 15
186 Phe Gly Pro Glu Glu Asp Ser Ser Tyr Leu Asp Gly Val Ser Leu Pro
187 20 25 30
188 Asp Phe Glu Leu Leu Ser Asp Pro Glu Asp Glu His Leu Cys Ala Asn
189 35 40 45
190 Leu Met Gln Leu Leu Gln Glu Ser Leu Ser Gln Ala Arg Leu Gly Ser
191 50 55 60
192 Arg Arg Pro Ala Arg Leu Leu Met Pro Ser Gln Leu Leu Ser Gln Val
193 65 70 75 80
194 Gly Lys Glu Leu Leu Arg Leu Ala Tyr Ser Glu Pro Cys Gly Leu Arg
195 85 90 95
196 Gly Ala Leu Leu Asp Val Cys Val Glu Gln Gly Lys Ser Cys His Ser
197 100 105 110
198 Val Ala Gln Leu Ala Leu Asp Pro Ser Leu Val Pro Thr Phe Gln Leu
199 115 120 125
200 Thr Leu Val Leu Arg Leu Asp Ser Arg Leu Trp Pro Lys Ile Gln Gly
201 130 135 140
202 Leu Leu Ser Ser Ala Asn Ser Ser Leu Val Pro Gly Tyr Ser Gln Ser
203 145 150 155 160
204 Leu Thr Leu Ser Thr Gly Phe Arg Val Ile Lys Lys Lys Leu Tyr Ser
205 165 170 175

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208 <210> SEQ ID NO: 6

209 <211> LENGTH: 176

210 <212> TYPE: PRT

211 <213> ORGANISM: Homo sapiens

213 <400> SEQUENCE: 6

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214 Ser Leu Glu Ser Ser Asp Cys Glu Ser Leu Asp Ser Ser Asn Ser Gly
215 1 5 10 15
216 Phe Gly Pro Glu Glu Asp Thr Ala Tyr Leu Asp Gly Val Ser Leu Pro
217 20 25 30
218 Asp Phe Glu Leu Leu Ser Asp Pro Glu Asp Glu His Leu Cys Ala Asn
219 35 40 45
220 Leu Met Gln Leu Leu Gln Glu Ser Leu Ala Gln Ala Arg Leu Gly Ser
221 50 55 60
222 Arg Arg Pro Ala Arg Leu Leu Met Pro Ser Gln Leu Val Ser Gln Val
223 65 70 75 80
224 Gly Lys Glu Leu Leu Arg Leu Ala Tyr Ser Glu Pro Cys Gly Leu Arg
225 85 90 95
226 Gly Ala Leu Leu Asp Val Cys Val Glu Gln Gly Lys Ser Cys His Ser
227 100 105 110
228 Val Gly Gln Leu Ala Leu Asp Pro Ser Leu Val Pro Thr Phe Gln Leu
229 115 120 125
230 Thr Leu Val Leu Arg Leu Asp Ser Arg Leu Trp Pro Lys Ile Gln Gly
231 130 135 140
232 Leu Phe Ser Ser Ala Asn Ser Pro Phe Leu Pro Gly Phe Ser Gln Ser
233 145 150 155 160

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234 Leu Thr Leu Ser Thr Gly Phe Arg Val Ile Lys Lys Lys Leu Tyr Ser
235                               165                      170          175
238 <210> SEQ ID NO: 7
239 <211> LENGTH: 191
240 <212> TYPE: PRT
241 <213> ORGANISM: Mus musculus
243 <400> SEQUENCE: 7
244 Met Val Ala Thr Gly Ser Leu Ser Ser Lys Asn Pro Ala Ser Ile Ser
245 1                               5                      10          15
246 Glu Leu Leu Asp Gly Gly Tyr His Pro Gly Ser Leu Leu Ser Asp Phe
247                               20                      25          30
248 Asp Tyr Trp Asp Tyr Val Val Pro Glu Pro Asn Leu Asn Glu Val Val
249                               35                      40          45
250 Phe Glu Glu Thr Thr Cys Gln Asn Leu Val Lys Met Leu Glu Asn Cys
251 50                               55                      60
252 Leu Ser Arg Ser Lys Gln Thr Lys Leu Gly Cys Ser Lys Val Leu Val
253 65                               70                      75          80
254 Pro Glu Lys Leu Thr Gln Arg Ile Ala Gln Asp Val Leu Arg Leu Ser
255                               85                      90          95
256 Ser Thr Glu Pro Cys Gly Leu Arg Gly Cys Val Met His Val Asn Leu
257                               100                     105         110
258 Glu Ile Glu Asn Val Cys Lys Lys Leu Asp Arg Ile Val Cys Asp Ala
259                               115                     120         125
260 Ser Val Val Pro Thr Phe Glu Leu Thr Leu Val Phe Lys Gln Glu Ser
261                               130                     135         140
262 Cys Pro Trp Thr Ser Leu Lys Asp Phe Phe Phe Ser Arg Gly Arg Phe
263 145                               150                     155         160
264 Ser Ser Gly Leu Lys Arg Thr Leu Ile Leu Ser Ser Gly Tyr Arg Leu
265                               165                     170         175
266 Val Lys Lys Lys Leu Tyr Ser Leu Ile Gly Thr Thr Val Ile Glu
267                               180                     185         190
270 <210> SEQ ID NO: 8
271 <211> LENGTH: 158
272 <212> TYPE: PRT
273 <213> ORGANISM: Drosophila melanogaster
275 <400> SEQUENCE: 8
276 Asn Leu Asp Asp Val Ser Ala Ser Ala Val Arg Glu Leu Ser Gln Gln
277 1                               5                      10          15
278 Leu Gln Ala Gln Leu Arg Asp Ala Lys Arg Arg His Leu Ala Cys Thr
279                               20                      25          30
280 Glu Val Thr Leu Pro Asn Asp Leu Thr Gln Arg Ile Ala Ala Glu Ile
281                               35                      40          45
282 Ile Arg Met Ser Glu Arg Glu Pro Cys Gly Glu Arg Ala Cys Thr Leu
283 50                               55                      60
284 Phe Ile Glu Phe Glu Ser Glu Pro Asn Lys Val Lys Arg Ile Ala Tyr
285 65                               70                      75          80
286 Phe Lys Val Asp Pro Asp Thr Val Ser Ile Phe Glu Leu Tyr Leu Thr
287                               85                      90          95
288 Leu Arg Gln Asp Lys Ser Gly Trp Ser Leu Thr Arg Ser Asn Thr Ile

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VERIFICATION SUMMARY

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